

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> Homogentisat-Dioxygenase

<130> M/40226

<140> 19937957.2

<141> 1999-08-11

<160> 15

<170> PatentIn Ver. 2.1

<210> 1

<211> 575

<212> DNA

<213> Brassica napus

<220>

<221> misc_feature

<222> (1)..(6)

<223> /function= "Restriktionsschnittstelle"

<220>

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<222> (570)..(575)

<223> /function = "Restriktionsschnittstelle"

<400> 1

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ctctttactg ctaaacaaga tttctctccg ttcaatgtgg ttgcctggca tggcaattac 180
gtgccttata agtatgacct gcacaagttc tgtccatata aactgtcctt tgtagaccat 240
ggagatccat ctgtaaatac agttctgaca gcaccaacgg ataaacctgg tgtggccttg 300
cttgattttg tcatattccc tcctcgttgg ttggttgctg agcatacctt tcgacctcct 360
tactaccatc gtaactgcat gagtgaattt atgggcctaa tctatggtgc ttacgaggcc 420
aaagctgatg gattttctacc tgggtggcgca agtcttcaca gttgtatgac acctcatggt 480
ccagatacaa ccacatacga ggcgacgatt gctcgtgtaa atgcaatggc tccttataag 540
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<210> 2

<211> 26

<212> DNA

<213> Künstliche Sequenz

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<223> Beschreibung der künstlichen Sequenz: /desc =
"Oligonukleotid"

<220>

<221> misc_feature

<222> (9)

<223> /mod_base = i

<220>
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 <222> (12)
 <223> /mod_base = i

<220>
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<220>
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 <222> (18)
 <223> /mod_base = i

<220>
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 <222> (21)
 <223> /mod_base = i

<220>
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 <222> (24)
 <223> /mod_base = i

<400> 2
 gtcgacggnc cnatnggngc naangg

26

<210> 3
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 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz: /desc =
 "Oligonukleotid"

<220>
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<220>
 <221> misc_feature
 <222> (24)
 <223> /mod_base = i

<220>
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 <222> (27)
 <223> /mod_base = i

<400> 3
 ggtacctcra acatraangc catngtncc

29

<210> 4
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 <213> Künstliche Sequenz

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<400> 4
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25

<210> 5
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 <213> Künstliche Sequenz

<220>
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<400> 5
 ggtaccgtga tagtaaaca ctaatg

26

<210> 6
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 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz: /desc =
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<400> 6
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<210> 7
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<400> 7
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<400> 8
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25

<210> 9
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<400> 9
 aagcttccga tctagtaaca taga

24

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<400> 10
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<210> 11
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 <213> Künstliche Sequenz

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<400> 11
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24

<210> 12
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 <213> Künstliche Sequenz

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<223> Beschreibung der künstlichen Sequenz: /desc =
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<400> 12

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<211> 32

<212> DNA

<213> Künstliche Sequenz

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<223> Beschreibung der künstlichen Sequenz: /desc =
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<400> 13

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<211> 1159

<212> DNA

<213> Künstliche Sequenz

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<223> Beschreibung der künstlichen Sequenz: /desc =
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<221> misc_feature

<222> (1)..(6)

<223> /function = "Restriktionsschnittstelle"

<220>

<221> CDS

<222> (8)..(1153)

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<222> (1154)..(1159)

<223> /function = "Restriktionsschnittstelle"

<400> 14

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1 5 10

gct gat cct ttt cca gtt aag gga atg gat gct gtt gtt ttc gct gtt 97
Ala Asp Pro Phe Pro Val Lys Gly Met Asp Ala Val Val Phe Ala Val
15 20 25 30

gga aac gct aag caa gct gct cat tac tac tct act gct ttc gga atg 145
Gly Asn Ala Lys Gln Ala Ala His Tyr Tyr Ser Thr Ala Phe Gly Met
35 40 45

caa ctt gtt gct tac tct gga cca gaa aac gga tct aga gaa act gct	193
Gln Leu Val Ala Tyr Ser Gly Pro Glu Asn Gly Ser Arg Glu Thr Ala	
50 55 60	
tct tac gtt ctt act aac gga tct gct aga ttc gtt ctt act tct gtt	241
Ser Tyr Val Leu Thr Asn Gly Ser Ala Arg Phe Val Leu Thr Ser Val	
65 70 75	
att aag cca gct acc cca tgg gga cat ttc ctt gct gat cac gtt gct	289
Ile Lys Pro Ala Thr Pro Trp Gly His Phe Leu Ala Asp His Val Ala	
80 85 90	
gaa cac gga gat gga gtt gtt gat ctt gct att gaa gtt cca gat gct	337
Glu His Gly Asp Gly Val Val Asp Leu Ala Ile Glu Val Pro Asp Ala	
95 100 105 110	
aga gct gct cat gct tac gct att gaa cat gga gct aga tct gtt gct	385
Arg Ala Ala His Glu Tyr Ala Ile Glu His Gly Ala Arg Ser Val Ala	
115 120 125	
gaa cca tac gaa ctt aag gat gaa cat gga act gtt gtt ctt gct gct	433
Glu Pro Tyr Glu Leu Lys Asp Glu His Gly Thr Val Val Leu Ala Ala	
130 135 140	
att gct act tac gga aag act aga cat act ctt gtt gat aga act gga	481
Ile Ala Thr Tyr Gly Lys Thr Arg His Thr Leu Val Asp Arg Thr Gly	
145 150 155	
tac gat gga cca tac ctt cca gga tac gtt gct gct gct cca att gtt	529
Tyr Asp Gly Pro Tyr Leu Pro Gly Tyr Val Ala Ala Pro Ile Val	
160 165 170	
gaa cca cca gct cat aga acc ttc caa gct att gac cat tgt gtt ggt	577
Glu Pro Pro Ala His Arg Thr Phe Gln Ala Ile Asp His Cys Val Gly	
175 180 185 190	
aac gtt gaa ctc gga aga atg aac gaa tgg gtt gga ttc tac aac aag	625
Asn Val Glu Leu Gly Arg Met Asn Glu Trp Val Gly Phe Tyr Asn Lys	
195 200 205	
gtt atg gga ttc act aac atg aag gaa ttc gtt gga gat gat att gct	673
Val Met Gly Phe Thr Asn Met Lys Glu Phe Val Gly Asp Asp Ile Ala	
210 215 220	
act gag tac tct gct ctt atg tct aag gtt gtt gct gat gga act ctt	721
Thr Glu Tyr Ser Ala Leu Met Ser Lys Val Val Ala Asp Gly Thr Leu	
225 230 235	
aag gtt aaa ttc cca att aat gaa cca gct ctt gct aag aag aag tct	769
Lys Val Lys Phe Pro Ile Asn Glu Pro Ala Leu Ala Lys Lys Lys Ser	
240 245 250	
cag att gat gaa tac ctt gag ttc tac gga gga gct gga gtt caa cat	817
Gln Ile Asp Glu Tyr Leu Glu Phe Tyr Gly Gly Ala Gly Val Gln His	
255 260 265 270	

att gct ctt aac act gga gat atc gtg gaa act gtt aga act atg aga 865
 Ile Ala Leu Asn Thr Gly Asp Ile Val Glu Thr Val Arg Thr Met Arg
 275 280 285

gct gca gga gtt caa ttc ctt gat act cca gat tct tac tac gat act 913
 Ala Ala Gly Val Gln Phe Leu Asp Thr Pro Asp Ser Tyr Tyr Asp Thr
 290 295 300

ctt ggt gaa tgg gtt gga gat act aga gtt cca gtt gat act ctt aga 961
 Leu Gly Glu Trp Val Gly Asp Thr Arg Val Pro Val Asp Thr Leu Arg
 305 310 315

gaa ctt aag att ctt gct gat aga gat gaa gat gga tac ctt ctt caa 1009
 Glu Leu Lys Ile Leu Ala Asp Arg Asp Glu Asp Gly Tyr Leu Leu Gln
 320 325 330

atc ttc act aag cca gtt caa gat aga cca act gtg ttc ttc gaa atc 1057
 Ile Phe Thr Lys Pro Val Gln Asp Arg Pro Thr Val Phe Phe Glu Ile
 335 340 345 350

att gaa aga cat gga tct atg gga ttc gga aag ggt aac ttc aag gct 1105
 Ile Glu Arg His Gly Ser Met Gly Phe Gly Lys Gly Asn Phe Lys Ala
 355 360 365

ctt ttc gaa gct att gaa aga gaa caa gag aag aga gga aac ctt tag 1153
 Leu Phe Glu Ala Ile Glu Arg Glu Gln Glu Lys Arg Gly Asn Leu
 370 375 380

gtcgac 1159

<210> 15

<211> 381

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz: /desc =
 "DNA"

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Met Thr Gln Thr Thr His His Thr Pro Asp Thr Ala Arg Gln Ala Asp
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Pro Phe Pro Val Lys Gly Met Asp Ala Val Val Phe Ala Val Gly Asn
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Ala Lys Gln Ala Ala His Tyr Tyr Ser Thr Ala Phe Gly Met Gln Leu
 35 40 45

Val Ala Tyr Ser Gly Pro Glu Asn Gly Ser Arg Glu Thr Ala Ser Tyr
 50 55 60

Val Leu Thr Asn Gly Ser Ala Arg Phe Val Leu Thr Ser Val Ile Lys
 65 70 75 80

Pro Ala Thr Pro Trp Gly His Phe Leu Ala Asp His Val Ala Glu His
 85 90 95

Gly Asp Gly Val Val Asp Leu Ala Ile Glu Val Pro Asp Ala Arg Ala
 100 105 110
 Ala His Ala Tyr Ala Ile Glu His Gly Ala Arg Ser Val Ala Glu Pro
 115 120 125
 Tyr Glu Leu Lys Asp Glu His Gly Thr Val Val Leu Ala Ala Ile Ala
 130 135 140
 Thr Tyr Gly Lys Thr Arg His Thr Leu Val Asp Arg Thr Gly Tyr Asp
 145 150 155 160
 Gly Pro Tyr Leu Pro Gly Tyr Val Ala Ala Ala Pro Ile Val Glu Pro
 165 170 175
 Pro Ala His Arg Thr Phe Gln Ala Ile Asp His Cys Val Gly Asn Val
 180 185 190
 Glu Leu Gly Arg Met Asn Glu Trp Val Gly Phe Tyr Asn Lys Val Met
 195 200 205
 Gly Phe Thr Asn Met Lys Glu Phe Val Gly Asp Asp Ile Ala Thr Glu
 210 215 220
 Tyr Ser Ala Leu Met Ser Lys Val Val Ala Asp Gly Thr Leu Lys Val
 225 230 235 240
 Lys Phe Pro Ile Asn Glu Pro Ala Leu Ala Lys Lys Lys Ser Gln Ile
 245 250 255
 Asp Glu Tyr Leu Glu Phe Tyr Gly Gly Ala Gly Val Gln His Ile Ala
 260 265 270
 Leu Asn Thr Gly Asp Ile Val Glu Thr Val Arg Thr Met Arg Ala Ala
 275 280 285
 Gly Val Gln Phe Leu Asp Thr Pro Asp Ser Tyr Tyr Asp Thr Leu Gly
 290 295 300
 Glu Trp Val Gly Asp Thr Arg Val Pro Val Asp Thr Leu Arg Glu Leu
 305 310 315 320
 Lys Ile Leu Ala Asp Arg Asp Glu Asp Gly Tyr Leu Leu Gln Ile Phe
 325 330 335
 Thr Lys Pro Val Gln Asp Arg Pro Thr Val Phe Phe Glu Ile Ile Glu
 340 345 350
 Arg His Gly Ser Met Gly Phe Gly Lys Gly Asn Phe Lys Ala Leu Phe
 355 360 365
 Glu Ala Ile Glu Arg Glu Gln Glu Lys Arg Gly Asn Leu
 370 375 380